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ALIGNMENTS

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Nucleotide sequence of the human Tcl-1b gene.
                                                                                 AAA75823;
                                                                                                                     AAA75823 standard; DNA; 6486 BP
                                       22-JAN-2001 (first entry)
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Tcl-1; Tcl-1b; T cell malignancy; chromosome 14 abnormality; lymphoma; T-cell leukaemia; immunodeficiency syndrome; ataxia-teleangiectasia; ss.

WO200055169-A1 Homo sapiens.

15-MAR-1999; 15-MAR-2000; 2000WO-US06612. 99US-0124714.

21-SEP-2000.

(UYJE-) UNIV JEFFERSON THOMAS.

Croce CM, Pekarsky Y;

WPI; 2000-611514/58.

Novel nucleic acid of Tcl-1 gene family, Tcl-1b, expressed in low levels in normal bone marrow and peripheral lymphocytes, but activated in T-cell leukaemia and lymphoma, used to identify chromosome 14 abnormalities

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tgcactccagcctgggcgacagagcaagact	ggcaggagaatggcttgaacctgggaggcg 	.caaaagaattagccgggtgcggtgcgggc 	aggtcaggagatcgagaccatcctggctaa 	gggcacggtggctcacgcctgaatcccagc 	acggttccacatgtcaatgcacttaatgcc 	agtaacaggtacggagtctcagtttgggaag 	cataaagtggaatggtagctgccaggggctg 	aaatatgccagtcacggaaggacagattctc 	aagtattcacccttaaaagtcagacacacg 	.aaaggtggtggcagccccgtgtccattga 	ccggaacttaagcatgtattcatacatcca 	aagaattacggcataatccagcaatgccac 	tggagggcactgtaaaatggtgcagccact 	agcatgcaaaaattgtggagcaaatattta 	ttatttcaaaaaatgttggtagagaacatgg 	cagccagttcactgacactttaaacaatata 	caagtgatctgcccaccttggcctcccaaag 	ורררה שא ל שא מא מה ממממ את ב ב ב ממ ב ב ב מי ב
	gagcttgcagtgagctga 294	tgtagtcccagctac 288	ct 282	ctttgggggaccgaggc 2/6 		ataaaaagttctggagg 264 	gagggagtcgaggatgg 258 	ttgtatgaggtactcag 252	gatgaaacttggagcca 246 	atgaatgggtaaac 240 atgaatgggtaaac 240	ω ω 4 4	∞ α	tggaaaacaggatgag 222 tggaaaacaggatgag 222	agtttttcaaaagcct 216 	aaaggcttttctgtac 210 aaaggcttttctgtac 210	acacatttcctaaaaa 204 	tgctgggattacaggt 198 tgctggattacaggt 198	799 CC 299 CC 299 CC 207 CC 20

021 tataagtgtgt 021 tataagtgtgt	Qy dd
3961 cccaaagtgttgggattacaggcataagccactgctcccagccttatttcgtatatttac 4020	Qy Db
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3661 tcatctttctaacttccagtaccagcctaattttgttatttttattattattgtatttatt	Qy Db
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gaaaat 360 gaaaat 360	Оу
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421 cagagaaggaqagattttgccgtataatttaaaatacttctcttttgcaaaagcagtccat 348 	Qу Db
1 tgcaaaagcagatgcaagccagacttagtttgctgatctctgatctacagtcagaataca 342 	Оу
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181 acacatctaatgcaaagatcagccacctttttctgtaaaggatctgatggtaaacatttt 32 	Qу
3121 ttccccttctttcttaaaaatagatcgatgtcttagggtgggaattaggcttcctgggcg 3180 	Qy Db
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The present sequence encodes a human Tc1-1b protein. The Tc1-1b gene is implicated in the development of T cell malignancies. Fragments of Tc1-1b cDNA sequences are used for detecting a target sequence indicating a chromosome 14 abnormality, such as a (14.14)(911:932) translocation or a (14)(911:932) inversion. Tc1-1b antisense sequences and antibodies are useful for treating a disease state such as T-cell leukaemia or lymphoma associated with a chromosome 14 abnormality. The Tc1-1b gene and its gene product are useful for treating disease states associated with the Tc1-1b locus on chromosome protein including T-prolymphocytic leukaemias, acute and chronic leukaemias associated with the immunodeficiency syndrome ataxia-teleangiectasia (AT).
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T-cell leukaemia; immunodeficiency syndrome; ataxia-teleangiectasia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of the human Tcl-1b cDNA.
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                                                                                                                                                                                                                                                                                    Novel nucleic acid of Tcl-1 gene family, Tcl-1b, expressed in low levels in normal bone marrow and peripheral lymphocytes, but activated in T-cell leukaemia and lymphoma, used to identify chromosome 14
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                                                RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation; diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoria benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
                                                                                                                           Retinoblastoma binding protein-7 genomic DNA sequence.
                                                                                                                                                             16-MAY-2000 (first entry)
                                                                                                                                                                                                                                 AAZ86967 standard; DNA; 162450 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              904 ccctgtgggtatcagttctgctgacactttggcccgaaatagatccagtgctgagcaagc 963
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                                    lymphoma;
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80316 AGTATATACCAAACAGAAACTATTTTTATTGAGACAGAATGTCACCCTATCATTCAGGCT 80257
                                                                              80376 AAATTCCATCTCAAAAAATAAAATAAAATTATTTGGAGGCAAAAACTGTCCTAAACTC 80317
                                                                                                                                                                 80436 GGCAGAGGTTGCGGTGAGCCAAGATTACACCATTGCACTCCAGCCTGTGCAACAAGAGCG
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                             1688 cgtaaacaattcactgcctgtttgtttttttttgagaaagtcttgctct-gttgcggct 1746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the retinoblastoma binding protein-7 (RBP-7) genomic sequence of the invention. The RBP-7 coding sequence and regulatory sequences are useful for the recombinant production of the protein and for expressing heterologous nucleic acids. Primers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 118-163; 223pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphomas. RBP-7 antibodies are useful as diagnostic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acid and polymorphic markers used for diagnosis of diseases, especially those involving abnormal cell proliferation and
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10-DEC-1998;
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                                                         79256 CCAAGGTGGGCGGATCACTTGAGGCTAGGAGTTCAAGACCAGCCTGGCCAACATGGCGAA 79197
                                                                                                                                                                   79311 C----AGATAATTGGCTGGGCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG 79257
                                                                                                                                                                                                                                                                             79431 AGAGGGAAAATGTCTATGGCCCTGTTACCTAAAATGGGCTGCAGAAAATATGGAACTGGG 79372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79491 AGCAAAAACCAGAGGCTCCTGAAAGCTGTATTAAAGGCACATAGAAAACTCCGTAGGCCT 79432
79551 TTTCAAGGGACTAAAAAGACCTGGGGGTAGGGTAGAATTTGTCCCATCTTAGACCTAAAG 79492
                                                                                          2754 ccgaggcgggcggatcaca--aggtcaggagatcgagaccatcctggctaacacggtgaa 2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79611 AGAAACATAAGCAATATCTCTGTCCCTATCTCAATGTCCAGGAAAGTAGGGGGCATGTTTG 79552
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                                                                                                                                                                                                    2695 tottaaaaacagttgaccgggcacggtggctcacgcctg-aatcccagcactttggggga 2753
                                                                                                                                                                                                                                                                                                                                    2635 tggaggtggatagtgccgacggttccacatgtcaatgccacttaatgccaccaaactgtac 2694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2335 gtatcattcatactagccaaaaggtggtggcagcccccgtgtccattgatagatgaatgg 2394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2156 agcctgaaaaagtgttaatggagggcactgtaaaatggtgcagccactatggaaaacagg 2215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78958 ATGAATGGTCTTTAGAAATACCTAAACTGTCCTACAGATG 78919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79018 AAAAATAAATAAATAAATAAATATCAGATGAATCTACTTTTGTATAAATACTCAAAGT 78959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79078 GTAAGCCAAGATCATGCCGCTGTACTCCAGTCTGGGCGACAGAGCAAGACTCTGTCTCAA 79019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tomato; monkey; dog; sea urchin; expressed sequence tag; ES diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2932 gtgagctgagatccagccactgcactccagcctgggcgacagagcaagactccgtctcaa 2991
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                                                The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human EST-derived coding sequence SEQ ID NO: 102.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JUL-2000;
03-AUG-2000;
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                                                                                                                                                                                             Claim 1; Page 246; 1275pp; English.
                                                                                                                                                                                                                                Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use - \,
                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
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2000US-0631451.
2000US-0663870.
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A, Zhang J, Werhman T;
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Sequence 697 BP; 135 A; 204 C; 181 G; 175 T; 2 other;

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Query Match 5.9%;
Best Local Similarity 83.7%;
Matches 493; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5885 tcccctgctggctgcaagctgtgggttc---tttctcctctgtgcccctcatgctgatctt 5942
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                                                                                                                                                                                                              Pigment epithelium-derived factor; PEDF; neuronal cells; neurons; glial cells; gliastatic; gliosis; central nervous system; CNS; neurodegenerative disease; injury; neuronotrophic; brain cells; Parkinson's disease; photorcceptor cells; retina; inhibition; proliferation; immunoassay; antibody; ageing; degenerative disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5766 cactcagtttctctcgtttttccttagttatcagtcctgtcctgtcctgtcccactcaggtctgta 5825
                                                                                                                                                                                                                                                                                                                                                                                                                 AAT11658 standard; DNA; 22481 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6058 gtttaagagatggcattagagggagcccagtctggatgtggacttggatgccctgtgggt 6117
                07-JUN-1994;
                                30-DEC-1994;
                                                               06-JUN-1995;
                                                                                                 14-DEC-1995
                                                                                                                                WO9533480-A1
                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                 PEDF full length sequence and flanking sequences.
                                                                                                                                                                                                                                                                                                                                                  16-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  AAT11658;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 at-agntctgctgacactgtggcctgaaatanaaaaagtgctgagcaagcagtgtatgct 628
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                94US-0367841
94US-0257963
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SOXCCCCCCCCCCCCCCXXX TTTTXXX TXXX
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13333 tagaga-tggggcctcaccatgttgctcaggttggtctgaaactcctgagctcaagtgat 13391
                                                                                                   13273 aaatagctgggaccacaggcacgtgccaccacgcccagctaattttttgggtatttttag 13332
                                                                                                                                                                                                       13213 tcttggctcactgcaatcttggcctcctgagttcaaccaattctcatgcctcagcctccc 13272
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                              1882 gagagacaaaagtttaatcatgtgggccaggctggttttgaactcctgacctcaagtgat 1941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1527 ctgtagtcccagctactcgggaggctgaggcaggagaatggcgtgaacccgggaggcgaa 1586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1347 ccggatatttaaáatgccatttagggctgggcgggtggctcacgcctgtaatcccagca 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and neural retina and photoreceptor cells. The gliastatic activit of PEDF can be applied to inhibiting glial cell proliferation in certain tumours. Antibodies directed against PEDF can be used for inhibiting PEDF activity or in an immunoassay for determining levels of PEDF in fluid, cellular or tissue samples e.g for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pigment epithelium-derived factor (PEDF) has both neuronotrophic and gliastatic activity, making it useful in cases where neurons die quickly and glia tend to proliferate (gliosis), e.g. in CNS cell culture, in neurodegenerative diseases and in CNS injury. The neuronotrophic effect of PEDF is especially useful for enhancing survival of neuronal cell cultures intended for use in transplantation. These include cultures of human foetal brain cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22481 BP; 5280 A; 5708 C; 6136 G; 5347 T; 10 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 100-122; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of pigment epithelium derived factor - for enhancing neuronal cell survival and inhibiting glial cell proliferation, useful, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            determining ageing and/or other degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in CNS cell culture or to treat neuro-degenerative diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gcttgtagtgagccgagatcgcaccactgcactccagcctgggtgacagagtgagactcc 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 357.6;
Pred. No. 2.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9e-69;
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AAH18348/c
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                                                                                                                                             the 5'-end sequence/3' end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs The primers allow obtaining of the full-length cDNAs of the primers allow obtaining of the full-length cDNAs of the primers allow obtaining of the full-length cDNAs represent human cDNA sequences; AAB92446 to AAB13633 to AAB13633 to AAB13643 represent human cDNA sequences; AB92446 to AAB13630 and AAB13633 to AAB13640 represent human cDNA sequences; AB92446 to AAB13630 and AAB13630 represent human cDNA sequences; AB92446 to AAB13630 and AB13640 represent human cDNA sequences; AB92446 to AAB13650 and AB13660 and
                                                                                                                                                                                                                                                                                                                                                                                                                         oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the polynucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
                                                                                      AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         full-length cDNAs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1436 agatcaggagatcgagaccatcctagccaacatggggaaaccccgtctctactaaaaaata 1495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1553 gaggcaggagaatggcgtgaacccgggaggcgaagcttgtagtgagccgagatcgcacca 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1548 CAAAAAAAATTAGCCAGGCGTGGTGGGGGATGCCTGTAGTCCCAGCTACTTGGGAGGTT 1489
                                                                                                                                                                                                                                                                                                                                                                                                     1957 tcccaaagtgctgggattaca--ggtgagccacctcgcccagcc 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1188 TACAGGCG-CCTGCCACCACACCCAGCTAATTTGTGTATTTTTAGTAGAGAC-AGGGTTT 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1308 TAGACAAAGTCTCACTCTGTCGCCCAGGCTGGAGTGCAATGGCATAATCTTGGTTCACTA 1249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 CACCATGCTGACCAGCCTGGTCTTGAACACCTGACCTCAGGTGATCTGCCCACCTAGGCC 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1897 aatcatgtgggccaggctggttttgaactcctgacctcaagtgatctgcccaccttggc 1956
                                                                                                                                                                                                Human AKAP10 gene SEQ ID NO: 36.
                                                                                                                                                                                                                                 12-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                   AAH02340 standard; DNA; 161425 BP.
              13-OCT-2000; 2000WO-US28413.
                                                                              WO200127857-A2
                                                                                                                 Homo sapiens.
                                                                                                                                                drug response; ds
                                                                                                                                                               Database; polymorphism; SNP; human; genetic marker; disease; infection;
                                                 19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACCTCCGCTTCCCGGGTTCAAGAGATTCTTCTGCCTCAGCTTCCCGAGTAGCTGGGAT 1189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  caacctccacctcccaggctcaagtgattctcatgcctcagcctcccgagtagcttggat 1836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  529;
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10-JUL-2000;
19-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4239 GGCCGGGTGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCAGGTGGA 4180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1371 ggctgggcgcggtggctcacgcctgtaatcccagcactttgggaggccgagatgggctta 1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 161425 BP; 47858 A; 33576 C; 34682 G; 45309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1431 tcacgagatcaggagatcgagaccatcctagccaacatggggaaaccccgtctctactaa 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 241-288; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and entering the information into a database -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-273865/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jurinke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SEQU-) SEQUENOM INC.
                                                                                                                                                                                                                                                                                                                        1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4119 AAATGCAAAAAAGTAGCCGGGCGTGGTGGCGGCGCCTATAGTCCCAGCTACTCGGGAGG 4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1491 aaatacaaaaaattagccgggcgtggtggcggacgcctgtagtcccagctactcgggagg 1550
                                                                                                                                                                                                                                                                                                                                                                             4059 CTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCAGAGCTTGCAGTGAGCCAAGATCACGC 4000
                                                                                                                                                                                                                                                                                                                                                                                                                                               1551 ctgaggcaggagaatggcgtgaacccgggaggcgaagcttgtagtgagccgagatcgcac 1610
3879 GTCTCTCTGTCACTCAGGCTGTGGCGCAGCATGACCACGGCTCACTGCAGTCTTGATC
                                                                                                                                                                                                                                              1728 gtcttgctctgttgcggctggagtgcactggtgtgatgttggctcactgcaacctccacc 1787
                                                                                                                                                                                                                                                                                     3759 GCCACCATGCCTGGTTAATTTTTTTTTTTTTTTTTGTAGAGAC-AGAGTTTTGCTATGTTGC 3701
                                                                                           1848 tttttttacagttaattttttttttgttattttcaggagagacaaaagtttaatcatgtggg 1907
                                                                                                                                          3819 TCCTGGGCTCAAGCAGTCCTCCTACTTCAAGCTTCCAGAGTAGCTGGGATTACAAGCATCT 3760
                                                                                                                                                                          1788 tcccaggctcaagtgattctcatgcctcagcctcccgagtagcttggattacaggcgatt 1847
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                                                                                                                                                                                                                                                                                                                    CACTGCACTCCAGCCTGGGCAACAGAGTGAGACTCCATCTCAAAACAACAACAACAACAAC 3940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCACGAGGTCAGGAGATCAAGACCATCCTGGCTAACACGGTGAAACCCCCATCTCTACTAA 4120
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2000US-0217658.
2000US-0663968.
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75.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 349.4; DB 22; Length Pred. No. 3.8e-67; 0; Mismatches 151; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 161425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rodi C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        He L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
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RESULT 8
AAH02339/c
                                                                                                                                                                                                            Query Match
                                                                                                                                                                                      Matches 476;
1551 ctgaggcaggagaatggcgtgaacccgggaggcgaagcttgtagtgagccgagatcgcac 1610
                                                  1491 aaatacaaaaaattagccgggcgtggtggcggacgcctgtagtcccagctactcgggagg 1550
                                                                                  4179 TCACGAGGTCAGGAGATCAAGACCATCCTGGCTAACACGGTGAAACCCCCATCTCTACTAA 4120
                                                                                                                                             1371 99ct999cgc9gt9gctcacgcctgtaatcccagcactttgggaggccgagatgggctta 1430
                                                                                               1431 tcacgagatcaggagatcgagaccatcctagccaacatggggaaaccccggtctctactaa 1490
                                                                                                                               4239 GGCCGGGTGCGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGAGGCCGAGGCAGGTGGA 4180
                                                                                                                                                                                                                                                             The present invention provides a database of human samples obtained from healthy individuals which can be used to identify polymorphic genetic markers. Data obtained for the database can be used to sort the samples by parameters such as age, sex and ethnicity. This is useful in linking markers with diseases, susceptibility to infection and drug responses. The present sequence was used in an assay to demonstrate the uses of the database of the invention.
                                                                                                                                                                                                                                      Sequence 162025 BP; 48006 A; 33691 C; 34805 G; 45523 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 196-241; 304pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Producing a database for identifying polymorphic genetic markers, comprises obtaining data relating to members of a healthy population
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-OCT-1999; 99US-0159176.
10-JUL-2000; 2000US-0217251.
10-JUL-2000; 2000US-0217658.
19-SEP-2000; 2000US-0663968.
                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-273865/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-OCT-2000; 2000WO-US28413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-APR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SEQU-) SEQUENOM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arug response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database; polymorphism; SNP; human; genetic marker; disease; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human AKAP10 gene SEQ ID NO: 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAH02339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH02339 standard; DNA; 162025
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                                                                                                                                                                                                Local
                                     AAATGCAAAAAAGTAGCCGGGCGTGGTGGCGGCGCCTATAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                                                                                                                                                                 entering the information into a database -
                                                                                                                                                                                              Similarity
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                                                                                                                                                                                    Conservative
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75.2%;
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                                                                                                                                                                                          .4; DB 22; Length 162025;
3.8e-67;
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14-JUL-2000;
26-JUL-2000;
26-JUL-2000;
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30-JUN-2000;
07-JUL-2000;
                          14-AUG-2000;
14-AUG-2000;
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07-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; breast antigen; ovarian antigen; cancer; metastasis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast or ovarian antigen genomic DNA SEQ ID NO: 256.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1788 tcccaggctcaagtgattctcatgcctcagcctcccgagtagcttggattacaggcgatt 1847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1671 aatgoogtttaggtottogtaaacaattoactgootgtttgtttgtttgttttt---gagaaa 1727
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2000US-0224518.
2000US-0224519.
2000US-0225213.
                                                               2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
2000US-0220964.
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2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215486.
2000US-021647.
2000US-0216880.
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Q
                                    Query Match 5.3
Best Local Similarity 57.3
Matches 981; Conservative
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
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08-NOV-2000;
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
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06-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
1366 tttagggctgggcgcggttggctcacgcctgtaatccca-gcactttgggaggccgagatg 1424
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17-NOV-2000;
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                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                            number of ovarian and AAI62467-AAI62572 and
                                                                                                                                                                                                                   The present invention
                                                                                                                                                                                                                                          Disclosure; SEQ ID NO: 256; 520pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                       WPI; 2001-488785/53.
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                                                                                             Sequence 32174 BP; 8001 A; 6837 C; 7064 G; 8747 T; 1525 other;
                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                  treating and/or preventing human diseases and disorders
                                                                                                                                                                                                                                                                       New isolated nucleic acids and polypeptides, useful for diagnosing,
                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                    their metastases. The present sequence is a genomic sequence of the
                                                                                                                                                                                  diagnosis, prevention
                                                                                                                                                          invention.
                                                                                                                                                                                                                                                                                                                               Barash SC,
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2000US-0249213
2000US-0249213
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2000US-0249216
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2000US-0254097.
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                                              5.3%;
                                                                                                                                                                                  provides the protein and coding sequences of a breast antigens. These are shown in AAM42240-AAM42345. The sequences can be used in the and treatment of breast and ovarian cancers, and
                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                   Score 343; DB 22;
Pred. No. 5.6e-66;
0; Mismatches 655;
                                                           Length 32174;
                                      Indels 75;
                                      Gaps
                                        17;
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14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

2000US-0232397. 2000US-0232398. 2000US-0232399. 2000US-0232400.

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2000US-0231244. 2000US-0231413. 2000US-0231414.

2000US-0231242. 2000US-0231243.

2000US-0229344. 2000US-0229345. 2000US-0229503. 2000US-0229513. 2000US-0230437. 2000US-0230438.

14-SEP-2000
21-SEP-2000
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25-SEP-2000
25-SEP-2000
26-SEP-2000
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2000US-0241826. 2000US-024617. 2000US-0246474. 2000US-0246475. 2000US-0246476. 2000US-0246476. 2000US-0246477. 2000US-0246478. 2000US-0246478. 2000US-0246478.

2000US-023401 2000US-0231663 2000US-0233663 2000US-0234223 2000US-0234274 2000US-0234283 2000US-0235484 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0236327 2000US-0236327 2000US-0236369 2000US-0236370 2000US-0236802 2000US-0236802 2000US-0236802 2000US-0236802 2000US-0237037 2000US-0237037 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0241786 2000US-0241786 2000US-0241786 2000US-0241786 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 14-AUG-2000; 18-AUG-2000; 22-AUG-2000; 22-AUG-2000; 23-AUG-2000; 23-AUG-2000; 21-SEP-2000; 01-SEP-2000; 01-SEP-2000;

2000US-0226868. 2000US-0227182. 2000US-0227009.

2000US-0226681.

2000US-0228924. 2000US-0229287. 2000US-0229343. 2000US-0225447. 2000US-0225757. 2000US-0225758. 2000US-0225759.

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15655 ggccgggtgtgggtccatgcctgtaatctcagcactttgggaggctgaagcaggtgga 15714
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                                                   2403 cacaaaccatgaagtattcacccttaaaagtcagacacacggatgaaacttggagccatt 2462
                                                                                                                                                          2343 catactagccaaaaggtggtggcagcccccgtgtccattgatagatgaatgggtaaacaa 2402
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19-MAY-2000; 07-JUL-2000;

2000US-0205515 2000US-0216880

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                                                                                                                                                                                                                                                                                                                          Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antifheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15955 aaaaaaaaaaaaaaaaagttacacctgtcggccgggtgcggcagctcacacctgtaatc 16014
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                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                       neurological disease; infection; nephrotropic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human genomic DNA SEQ ID NO 232.
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29-SEP-2000;
13-OCT-2000;
                                                                    14577 tgtactggctggtgcagtggctcacgcctgtaaaccaaggcactttgggaggctgaggtg 14636
14637 ggtggatcacttgagatccggagtttgagaccatactggccaacatggtgaaaccccatc 14696
                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes (AAI62752-AAI62961) and proteins (AAM62347-AAM42415) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e:g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel plasma membrane associated proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancer, immune response and neuronal disorders
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06-SEP-2000;
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                 1425 ggcttatcac--gagatcaggagatcgagaccatcctagccaacatggggaaaccccgtc 1482
                                                                                     1366 tttagggctgggctgggctcacgcctgtaatccca-gcactttgggaggccgagatg 1424
                                                                                                                                                                                                                                                                                                                            disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
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                                                                                                                                                                                                                         Sequence 32174 BP; 8001 A; 6837 C; 7064 G; 8747 T; 1525 other;
                                                                                                                                                                                                                                                                           Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                               and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                              (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes meilitus, Cro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; SEQ ID NO 232; 532pp + Sequence Listing; English.
                                                                                                                                                                                                                                                           from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                   Match 5.3%;
Local Similarity 57.3%;
                                                                                                                                        981;
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2000US-0251990.
2000US-0254097.
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                                                                                                                                                     Score 343; DB 22; Length 32174; Pred. No. 5.6e-66;
                                                                                                                                          Mismatches 655; Indels 75; Gaps
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2523 tggtctcattcataaagtggaatggtagctgccaggggctg-----gagggagt 2571
                                                                                                                   2463 atactaaatgaaatatgccagtcacggaaggacagattctcttgtatgaggtactcagag 2522
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Example 8; Page 99-104; 226pp; Japanese.

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                      Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
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                                                                                                         WPI; 2001-226686/23.
                                                                                                                                                                                    (CHIB-) CHIBA PREFECTURE
                                                                                                                                                                                                     (HISM ) HISAMITSU PHARM CO LTD.
                                                                                                                                                                                                                                         09-MAY-2000; 2000JP-0136266.
                                                                                                                                                                                                                                                            31-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                   08-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour suppressor; human 1p36 homozygosity deletion domain; tumour
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                                                                                                                                                                                                                                                            99JP-0245962
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6458 accgcgcccagctccatttctgatgtgttccaatatttca 6497
                                  1986 acctcgcccagccagttcactgacactttaaacaatataa 2025
                                                                                                    6398 tgacctcaagtgatacacctgccttggcctcccaaagtgctgggattacaagtgggagcc 6457
                                                                                                                                 1928 tgacctcaagtgatctgcccaccttggcctcccaaagtgctgggattacaggt--gagcc 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36) in human neuroblastoma. Also described are base sequences from the 1p36 position of human neuroblastoma cell lines (NB-1 and MASS-NB-SCH-1), which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes in human neuroblastoma. The genes are tumour markers and reagents in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAF97787 to AAF9789 represent PCR primers used in the exemplification of the present invention, and AAF9780 to AAF97874 represent sequences given in the exemplification of the present nvention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5980 tcctagctactcaggaggctgaggcaggagaatggcgtgaacctgggaggtggagcttgc 6039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13927 BP; 3640 A; 2824 C; 3150 G; 4305 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 5.2%;
Local Similarity 73.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes the coding and protein sequences of the human kinesin-like protein HKLP. It is thought that the protein could be involved in neurological disorders, infertility, spontaneous abortion, neonatal chromosome disorders, aneuploidy and cancers. This is due to its function in the movement of microtubules. The protein shows homology to the murine KIFIA and KIFIB proteins. The sequences disclosed in the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in the invention that it is the interval of the invention can be used in the isolation of similar human proteins and in vector production. In addition, the biallelic markers shown can be used in the interval of the inventor in the interval of the interval 
                                                                                                                                                                                                                                     1533 tcccagctactcgggaggctgaggcaggagaatggcgtgaacccgggaggcgaagcttgt 1592
                                                                                                                                                                                                                                                                                                                                                                          1474 aaccccgtctctactacaaatac-aaaaattagccgggcgtggtggcggcgcctgtag 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1414 aggccgagatgggcttatcacgagatcaggagatcgagaccatcctagccaacatgggga 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3175 ttaaaaagagctttcatggccaggcgcggtggctcacgcttgtaatcccagcactttggg 3234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1354 tttaaaatgccatttagggctgggcgcggtggctcacgcctgtaatcccagcactttggg 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An isolated or purified human kinesin-like protein (HKLP) encoding polynucleotide used to detect HKLP polynucleotides in a sample comprises a contiguous span of at least 12 nucleotides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; kinesin-like protein; HKLP; KIF1; cell division; cancer; intracellular transport; neurological disorder; infertility; biallelic marker; spontaneous abortion; neonatal chromosome disorder;
1653 aaaaaaaaaaaaaaaaaaaa-------tgccgtttaggtcttcgt 1690
                                                                                                   1593 agtgagccgagatcgcaccactgcactccagcctgggtgacagagtgagactccgtccca 1652
                                                                                                                                                                                                   3355 tcctagctactcaggaggctgaggcaggagaatggcgtgaacctgggaggtggagcttgc 3414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3235 aggccgaggcgggggatcacaaggtcaggagatcaagaccatcctggctaacacggtga 3294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121162 BP; 33272 A; 24108 C; 25842 G; 37919 T; 21 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 143-175; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-665242/64.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aneuploidy; ds.
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                                                              3415 agtgagccgagatcgtgccactccccttcagctagggcgacagagggagactctgtctca 3474
                                                                                                                                                                                                                                                                                                                                     3295 aaccccgtctctactaaaaatacaaaaaaattagctgggcgtggtggtggcggcctgtag 3354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in disease diagnosis and population studies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 5.2%; Score 340.4; DB 21; Length 121162; Local Similarity 73.4%; Pred. No. 3.4e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0130217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; SPG4 gene; spastin; PSF-AD; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of the human SPG4 gene.
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95143 ACTGCAACCTCTGCCTCCCAAGTTCAAGTGATTCTCCTGCCTCAGCTTCCCAAGTAGCCA 95084
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                                                                                             95203 TTTTGAGACTGGGTCTCACTCTGTCGCCCAGGCTAGAGTGCAATGGGGGCAATCTTGGCTC 9514
                                                                                                                                                                                     95323 AATTAATTAAAAAAATAAAGGTTATTGAAAAACAAAATAGAACATTATTAAAGGATTAAC 95264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95623 GGCCAGGCATGGTGGCTCACGCCTGTAATCCTTGCACTTAGGGAGGCCGAGGCTGGCGAT 95564
                    1773 actgcaacctcccacctcccaggctcaagtgattctcatgcctcaggcttcacgagtagctt 1832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1542 ctcgggaggctgaggcaggagaatggcgttgaacccgggaggcgaagcttgtagtgagccg 1601
                                                                                                                   1716 ttttttgagaaagtcttgctctgttgc---ggctggagtgcactggtgtgatgttggctc 1772
                                                                                                                                                                                                                                1697 -----ttcactgcctgtttgtttg 1715
                                                                                                                                                                                                                                                                                                                                                                                                      1490 aaaatac-----aaaaaattagccgggcgtggtggcggacgcctgtagtcccagcta 1541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1371 ggctgggcgcggtggctcacgcctgtaatcccagcacttttgggaggccgagatgggct-t 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encode spastin (particularly sequences in other mammals, specifically mice); to identify SPG4 mutations, or other genetic anomalies, particularly for diagnosis of autosomal dominant familial spastic paraplegia (PSF-AD); to identify promoters and other regulatory elements of the SPG4 gene; for detection and amplification; for recombinant production of spastin; and for diagnostic genotyping of PSF-AD.
                                                                                                                                                                                                                                                                                                                             1662 aaaaaaaaaaatgccgtttaggtcttcgtaaacaa------1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1430 atcacgagatcaggagatcgagaccatcctagccaacatggggaaaccccgtctctacta 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a human SPG4 gene. The SPG4 gene encodes a spartin polypeptide. Mutations in the SPG4 gene are responsible for autosomal dominant familial spastic paraplegia. SPG4 polypuclaebtides, and their fragments, are used to screen DNA banks for sequences that and their fragments, are used to screen DNA banks for sequences that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 110000 BP; 30622 A; 21640 C; 22817 G; 34921 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 45-106; 145pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human nucleic acid from the SPG4 gene, useful e.g. for diagnosis of autosomal dominant familial spastic paraplegia and in drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weissenbach J, Hazan J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 Match 5.2%; Score 338; DB 22; Length 110000; Local Similarity 51.2%; Pred. No. 1.1e-64; hes 1458; Conservative 0; Mismatches 1171; Indels 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-283966/30.
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exon

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2737 94127	4 ctcttaaaaacagttgaccgggcacggtggctcacgcctg-aatc 	269 9418	Фу
2693 94187	4 ctggaggtggatag 6 GTCAAGGCTACAGT	263 9424	dq Qy
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2573 94307	4 tactcagagtggtctcattcattaaagtggaattggtagctgccagggggctggagggag	251 9436	ру
2513 94364	id tactaaatgaaatatgccagtcacggaaggacagattctcttgtatgagg	246 9442	Оу
2463 94424	4 acaaaccatgaagtattcacccttaaaagtcagacacacggatgaaacttggagccatta 	240 9448	Qy Db
2403 94484	4 atactagccaaaaggtggtggcagcccccgtgtccattgatagatgaatgggtaaacaac	234 9454	Qy Db
2343 94544	4 gactctgaagccggaacttaagcatgtattcatacatccatgttcacagcagtatcattc	228 9460	Db Qy
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2223 94664		216 9472	Оу
2164 94724	5 actaaataaagcatgcaaaaattgtggagcaaatattttaagtttttcaaaagcctgaaa	210 9478	Qу рь
2104 94784	5 tcaaataggttatttcaaaaaatgttggtagagaacatggaaaggcttttctgtacatac	204 9484	Оу
2044 94844	5 cacctogcccagccagttcactgacactttaaacaatataacacatttcctaaaaaaagt	198 9490	Оу
1984 94904	7 ctgacctcaagtgatctgcccaccttggcctcccaaagtgctgggattacaggtgagc	192 9496	Ф
1926 94964	3 gtttaatcatgtgggccaggctggttttgaactc 	189 9502	Qу
1892 95024	3 ggattacaggcgatttttttttacagttaattttttttgttattttcaggagagacaaaa GGACCACAGGCACGTGCCCAGCTATTTTTTTTTTTTTTT	183 9508	DB 04

3873 tttt-tattttttgtagagacagagtctcattatgttgccgaggctggtcttgaactcgt 393	Qy
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167 CTTGTTCTTTACAAAATGCATTAGTCTTTTTTTTTTTTT	Db
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	рь
cagacttagtttgctgat	Qy
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3333 cttagtttatttacaataaagctttatttgcaaaagcagatgcaa 337	Qy
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TCCAC	Db
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94007 TGGGCGCCTGTAGTCCCAGCTACTAGGGAGGCTGAGGCAGGAGAATGGCGTGAACCCGGG 939	Db
cgtctgtagtcccagctactcggggggctgaggcaggagaatggcttgaac	Qy

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RESULT 14
AAD08215
                                                                 The invention relates to human DNA helicase protein, NHL and its corresponding DNA molecule. NHL gene is localised on human chromosome 20 (20q13.3). NHL protein and its DNA are useful for treating various neoplastic disorders and genetic disorders such as multiple sclerosis, including xeroderma, pigmentosum, Cockayne's syndrome, Bloom's syndrome and Werner's syndrome. NHL protein is useful for selecting compounds active against neoplastic disorders. NHL protein is useful for screening and measuring levels of NHL, and for formulating kits suitable for detecting and typing NHL. The invention also relates to a method for identifying modulators of NHL activity. The present DNA sequence is human genome from BAC clone, hbm168. This human genomic DNA contains %68/DcR3, NHL DNA helicase, SCLIP and ARP gene at chromosome location of ACC and ARP servers and AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92940 TITTGTATTTCAGTAGAGATGCGGTTTCACCATATTGGCCAAGCTGGTCTCGAACTCCT 92881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polynucleotide encoding mammalian DNA helicase, NHL, useful for screening and measuring levels of NHL, and for formulating kits suitable for detecting and typing NHL - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 23; Page 21-78; 169pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genetic disorder; multiple sclerosis; pigmentosum; Cockayne's syndrome;
Bloom's syndrome; Werner's syndrome; therapy; chromosome 20; м68/DcR3;
SCLIP; ARP; BAC clone hbm168; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; DNA helicase; NHL; cytostatic; neoplastic disorder; xeroderma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genome from BAC clone, hbm168.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Corresponds to human DNA helicase, NHL gene" 48688..84857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "Human DNA helicase, NHL"
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Sequence 114793 BP; 24123 A; 32916 C; 31886 G; 25868 T; 0 other;

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AAF97862
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Best Local Similarity 75.3%;
Matches 492; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62802 cttggcctcccaaagtgctgggattacaggtgtgagccaccgcgcccggcctg 62854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62742 ggggtttccccagcgttgcccaggctggtcttgaacccctgagctcaagtgatctgcccac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62684 ccgggactacaggtgcacaccaccacgcccggctaatttttgtattttt--tgtagaggc 62741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62564 gtttgttgagacagggtctccttctgtcgtccaggctggagttcagtggtatgatcttgg 62623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1950 cttggcctcccaaagtgctgggattacag--gtgagccacctcgcccagccag 2000
                   31-AUG-2000; 2000WO-JP05930
                                                                        08-MAR-2001.
                                                                                                                           WO200116311-A1
                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                   tumour suppressor; human 1p36 homozygosity deletion domain; tumour;
                                                                                                                                                                                                                                                                            Human; chromosome 1; 1p36; neuroblastoma cell line; NB-1; anticancer;
                                                                                                                                                                                                                                                                                                                            Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:76.
                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF97862 standard; DNA; 22081 BP
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31-AUG-1999;

99JP-0245962

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12085 ggcacatgcccgtagaaccagcgactcgggaggctgagacaggaggaaccacctgaattc 12144
12385 agcgatcctcccacctcagcctgccacctagctgggatcataggtgtgcaccactgcgcc 12444
                                                                                             12325 ccgaggctggagtacagtggtggtggtcatgggtcactgcaacctccatctcctgggctta 12384
                                                                                                                                                                                                                                                                                      12205 caagacccagtctaaaaaaaaccaccactgctccaggggtccaggggtcaggcacactc 12264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which are tumour suppressor genes in human neuroblastoma. The genes are tumour suppressor genes, base sequence data of which are applicable as tumour markers and reagents in studying mechanism of tumour body formation, and gene diagnosis of tumours as well as in developing anti-cancer drugs. AAF9787 to AAF97829 represent PCR primers used in the exemplification of the present invention, and AAF97830 to AAF97874 represent sequences given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human 1p36 homozygosity deletion domain from the 36-position of first chromosome short arm in human neuroblastoma cell lines, applicable e.g. in gene diagnosis of tumors as well as in developing anti-cancer drugs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes a homozygosity deletion domain co-existing in the 36-position of the first chromosome short arm (1p36)
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                          1740 -tgcggctggagtgcactggtgtgtgttgtgtctactgcaacctccaacctcccaggctca 1798
                                                                                                                                                                                                                                       1682 ggtcttcgtaaacaattcactgcctgtttgtttgtttttttgagaaagtcttgctctgt-- 1739
                                                                                                                                                                                                                                                                                                                                     Sequence 22081 BP; 5910 A; 5508 C; 5430 G; 5233 T; 0 other
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Db 13462 ccaagaccacgccactgcactccagcctgggtgacagagcgagactctgtctcaaaaaaa 13521

Search completed: November 29, 2001, 09:34:35 Job time: 19671 sec

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                     4.1.14796
4.0.7517
4.0.75231
4.0.246240
4.0.246240
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4.0.246240
4.0.246240
4.0.246243
3.9.176373
3.9.176373
3.9.13158
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Copyright (c) 1993 - 2000 Compugen Ltd.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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PCT-US95-07201-43
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PCT-US95-078-294-12
PCS-08-14-095-7
PCT-US93-052-18
PCS-08-124-394A-22
PCS-08-124-394A-22
PCS-08-125-17
PCT-US93-0525-18
PCS-08-724-394A-20
PCS-08-724-394A-20
PCS-08-724-394A-20
PCS-08-724-394A-21
US-09-299-549-1
US-08-781-891-79
US-09-128-155-17
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US-09-385-982-128
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7544.614 Million cell updates/sec
Sequence 1, Appli
Sequence 79, Appl
Sequence 17, Appl
Sequence 105, App
Sequence 128, App
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7, Appli
12, Appl
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Appli
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Sequence 102, App							
Ü	US-08-742-185-102	w	40328	ω &	249.2	45	C
-	US-09-058-389A-5	ω	6354	3.8	249.4	44	C
Sequence 12, Appl	US-09-058-389A-12	ω	1712	3.8	249.4	43	C
Sequence 3, Appl	US-09-077-354B-3	4	10380	3.8	249.6	42	
Sequence 7, Appl	US-09-503-444A-7	4	10825	3.9	250.8	41	
Sequence 5, Appli	US-09-503-444A-5	4	10825	3.9	250.8	40	
Sequence 3, Appli	US-09-503-444A-3	4	10825	3.9	250,8	39	
Sequence 1, Appl	US-09-503-444A-1	4	10825	3.9	250.8	38	
Sequence 7, Appl	US-08-834-497A-7	ω	10825	3.9	250.8	37	
Sequence 5, Appli	US-08-834-497A-5	w	10825	3.9	250.8	36	
Sequence 3, Appli	US-08-834-497A-3	ω	10825	3.9	250.8	35	
Sequence 1, Appl	US-08-834-497A-1	ω	10825	3.9		34	
Sequence 7, Appli	US-08-652-265-7	w	10825	3.9	250.8	ω ω	
Sequence 5, Appli	US-08-652-265-5	ω	10825	3.9		32	
Sequence 3, Appli	US-08-652-265-3	w	10825	3.9	250.8	31	
Sequence 1, Appl	US-08-652-265-1	ω	10825	3.9	250.8	30	
Sequence 33, App	PCT-US94-07926-33	σ	15328	3.9	254.4	29	
Sequence 33, App	US-08-888-497-33	N	15328	3.9	254.4	28	

ALIGNMENTS

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PCT-US95-07201-43
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                                                                                                                       TELEFAX: (212) 751-68
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Chader, Gerald J.; Becerra, Sofia
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PICKENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 30-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                           FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/9
FILING DATE: 24-SEP-1992
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 07-JUN-1994
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MOLECULE TYPE: Genomic DNA
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                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION:
                    STRANDEDNESS:
TOPOLOGY: Un
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                           REGISTRATION NUMBER: 36434
                                                                            LENGTH:
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                                                          H: 22481 Base Pairs
Nucleic Acid
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                                                                                                                                            (212) 751-6849
                      Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                   13392 CCATCTTCCTCGGCCTGCCAAAGTGCTGGGATTATAGG 13429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13213 TCTTGGCTGCAATCTTGGCCTCCTGAGTTCAACCAATTCTCATGCCTCAGCCTCCC 13272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13333 TAGAGA-TGGGGCCTCACCATGTTGCTCAGGTTGGTCTGAAACTCCTGAGCTCAAGTGAT 13391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13273 AAATAGCTGGGACCACAGGCACGTGCCACCACGCCCAGCTAATTTTTTGGGTATTTTTAG 13332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12856 CTTTGGGAGGTGGAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAAC 12915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13153 CTTTCTTTTTTAGAGACAGAGTCTCACTCCATCACCCATGCTGGAGTACAGTGGTGCGA 13212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13036 GGTTGCAGTGAGCTGAGCTCGCACCACTGCACTCCAGCCTGGGCGACAGAGTGAGACTCC 13095
                                                                                                                  TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
                                                                                                                                                                                          APPLICANT: Chader, Gerald J.; Becerra, Sofia APPLICANT: Patricia; Schwartz, Joan P.; APPLICANT: Taniwaki, Takayuki
                                                                                                                                                                                                                                                                                                                                                                                                                                              1942 ctgcccaccttggcctcccaaagtgctgggattacagg 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1882 gagagacaaaagtttaatcatgtgggccaggctggttttgaactcctgacctccaagtgat 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1707 gtttgtttgtttttgagaaagtcttgctctgttgc---ggctggagtgcactggtgtga 1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12916 ACGGTGAAACCCCCGTCTCTACTAAAAATACAAAAATTAGCTGGGTGTGGTGGGGGGGCGC 12975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1407 ctttgggaggccgagatgggcttatcacgagatcaggagatcgagaccatcctagccaac 1466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1764 tgttggctcactgcaacctccacctcccaggctcaagtgattctcatgcctcagcctccc 1823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1587 gcttgtagtgagccgagatcgcaccactgcactccagcctgggtgacagagtgagactcc 1646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1467 atggggaaaccccgtctctactaaaaatacaaaaaattagccgggcgtggtggtggcgc 1526
                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1647 gtcccaaaaaaaaaaaaaaaaaaaaatgccgtttaggtcttcgtaaacaattcactgcct 1706
                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
CITY: New York
                          STREET:
                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: full length genomic OTHER INFORMATION: sequence for PEDF plus flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION METHOD:
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                          345 Park Avenue
                                               Morgan & Finnegan, L.L.P.
                                                                                                    43
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 490; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                              13350 GGTGAGGCCCCATCTCTACTAAAAATACCCCAAAAATTAGCTGGGCGTGGTGGCACGTGC 13291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                               13290 CTGTGGTCCCAGCTATTTGGGAGGCTGAGGCATGAGAATTGGTTGAACTCAGGAGGCCAA 13231
                                                                                                                                                                                                                                                                                                                                                                                                 13410 GGCAGGCCGAGGAAGATGGATCACTTGAGCTCAGGAGTTTCAGACCAACCTGAGCAACAT 13351
1707 gtttgtttgtttttgagaaagtcttgctctgttgc---ggctggagtgcactggtgtga 1763
                                                                                                                                                                                                                                             1527 ctgtagtcccagctactcgggaggctgaggcaggagaatggcgtgaacccgggaggcgaa 1586
                                                                                                                                                                                                                                                                                                                                 1469 ggggaaaccccgtctctactaaaaata--caaaaaattagccgggcgtggtggcggacgc 1526
                                                                                                                                                                                                                                                                                                                                                                                                                      1411 gggaggccgagatgggcttatcac--gagatcaggagatcgagaccatcctagccaacat 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1351 atatttaaaatgccatttagggctgggctgggctcacgcctgtaatcccagcacttt 1410
                                                                    | 1647 gtcccaaaaaaaaaaaaaaaaaaaaaaatgccgtttaggtcttcgtaaacaattcactgcct 1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 24-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: full length genomic OTHER INFORMATION: sequence for PEDF plus flanking sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/257,963 FILING DATE: 07-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 4.8%; Score 313.8; DB 5; Length 22481; Local Similarity 74.6%; Pred. No. 9.3e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: P1-147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10154
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IBM PC Compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 758-4800
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US-08-781-891-79
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Patent No. 6090620
                                                                          Matches
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INFORMATION FOR SEQ ID NO: 75
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12933 GAGAC-GGGGTTTCACCGTGTTAGCCAGGATGGTCTCGATCTCCTGACCTC--GTGATCC 12877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13053 GCTCAGCTCACTGCAACCTCCACCTCCCGGGTTCACGCCATTCTCCTGCCTCAGCCTCCC 12994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   NAME: No. 6090620tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                          Local Similarity
                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Yu, Chang-En
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                                                                          Conservative
                                                                                                                                                                                       linear
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                                                                                                                                                                                                      single
                                                                                          4.8%; Score 309.4; DB 3; Length 87350; 72.6%; Pred. No. 3.4e-71;
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US-08-814-095-7/c
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Patent No. 6025183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30043 TAATTTTTGTATTTT--AGTAGAGATGAGGTTTCACTGTGTTGTCCAGGCTGGTGTTGA 30100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1745 ctggagtgcactggtgtgatgtt--ggctcactgcaacctccacctcccaggctcaagtg 1802
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                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1983 g 1983
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: KOHN & AS
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ATTORNEY/AGENT INFORMATION:
                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                ZIP: 48334
                                                                                                                                                                                                                                                                                                                         CITY: Farmington Hills
                                                                                                                                                                                                                                                                                              Michigan
                                                                                                                                                                                                                                                                                                                                              E: KOHN & ASSOCIATES 30500 No. 6025183thwestern Highway, Suite 410
                                                                                                                                                                                                                                                                        U.S.
                                                                        US/08/814,095
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TELEPHONE: (248) 539-5050
TELEPAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FEATURE:
                                                                                                                                 FEATURE:
                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                FEATURE
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DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
      IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE" OTHER INFORMATION: /number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
                                                                                                                                                                                               OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE" OTHER INFORMATION: /number= 5
                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE"
                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /gene= "ACHE"
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LOCATION: 25524..26009
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OTHER INFORMATION: 241
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OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
                                                                                                                                               LOCATION:
                                                                                                                                                                   NAME/KEY:
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LOCATION:
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LOCATION: 22465..22537
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OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: promoter LOCATION: 4089..22464
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27255..28007
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27005..27274
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                                                                                      LUCATION: complement (30470..30626)
OTHER INFORMATION: /gene= "AR"
LOCATION: complement (30187..30274) OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
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   9324 TTTTCTTTATAAATCACCCAGTCTTAGGCATTTATAGCAATGCAAGAATGGCCTAACACG 9265
                                                   2144 aagtttttcaaaagcctgaaaaagtgttaatggagggcactgtaaaatggtgcagccact 2203
                                                                                                          9384 AGCAAATGCTGGCACCGTGCTTCCTGTACAGCCTGCAGAACCGTGAGCCAAATAAACTTT 9325
                                                                                                                                                             2085 aaaggcttttctgtacatacactaaataaagcatgcaaaaat-tgtggagcaaatatttt 2143
                                                                                                                                                                                                                          9444 ACATGCCAGCTCCCCTTCAACTTCCCCTGTAAGTGGAAGCTTCCTGAGGTCCTCACCAGA 9385
                                                                                                                                                                                                                                                                           2025 acacatttcctaaaaaaagttcaaataggttatttcaaaaaatgttggtagagaacatgg 2084
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Local Similarity 48.6%; Pred. No. 5.6e-71;
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OTHER INFORMATION: /gene= "ARS"
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                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08814095 Patent No. 6025183
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                    APPLICANT: Soreq, Hermon
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                               TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTNACES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3949 ctgccttggcctcccaaagtgttgggattacaggcattaagccactgctcccagccttatt 4008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7406 CTTCTATCTAATTGTATTTTTGT 7384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4009 tcgtatatttactataagtgtgt 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3889 agacagagtctcattatgttgccgaggctggtctttgaactcgtggcttcnagcagtcctc 3948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3830 gagtagctgggactgtaggcacatggccaccatggccagctaattttt-tattttttgtag 3888
STREET: 30500 No. CITY: Farmington STATE: Michigan
                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7466 CCGCCTCGGCCTCCCAAAGTGCTATGATTACAGGCATGAGCCACTGTGCCCGGCCTATTT 7407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7526 AGATGAGGTTTCACCATGTGGGCCAGGCTGGTCTTGAATTCCTGACTTCAGGTGATCCAC 7467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7586 GAATAGCTGGGATTACAGGCACATGCCACCACCACCGGCTAATTTTTGTAATTTTAGTAG 7527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7646 TCTTGGCTCACTGCAACCTCCGCCTCTTGAGCTCAAGCGATTCTCCTGCCTCAGCCTCCT 7587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3770 cgatagettacaacageetetaceteceaggttcaagaaatetteteacettagetteec 3829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7706 TTTTTTTTTTTTTAGGCGGAGTCTCACTCTGTCACCCAGGCTGAAGTGCAATGACGCAG 7647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3710 atgtatttattttgagacagagtcttgctctgtctcccaggctggagtgcagtgacctga 3769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7766 TAAAATGCTGGTGATTGTGGAGGACTTTGTTTTTTGCTTCCTGTTTTTCAATTTCCTTTT 7707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3650 tacttttcctatcatctttctaacttccagtaccagcctaattttgttatttttattatt 3709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3552 taattcaaaaagacattttatcacaaaagaagacaaatacttagaaaattgtgcaaaaga 3611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8065 ATTAAGGGAATGCAGTCTTTTAATCAGAACTCTGCCAATGCTTTTTATCTAGATGCCTAT 8006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3267 tactcag------ctctgctattgcagtgcaaaagcagctaaaggcaaccgg 3311
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                               Farmington Hills
                                                                                                                                                                                                                                                                        Soreq, Hermona
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TELEFAX: (248) 539-50 INFORMATION FOR SEQ ID NO:
                                                                                                     FEATURE
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DESCRIPTION: /desc = "Cosmid including ACHE
DESCRIPTION: promotor, ACHE gene and ARS ger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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LENGTH: 35060 base pai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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OTHER INFORMATION: /ev
OTHER INFORMATION: /ge
OTHER INFORMATION: /evidence- EXPERIMENTAL OTHER INFORMATION: /gene- "ACHE"
                                                          NAME/KEY: exon
LOCATION: 27255..28007
                                                                                                                   OTHER INFORMATION: OTHER INFORMATION:
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                                        IDENTIFICATION METHOD:
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                                                                                                                                                                          NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
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LOCATION: 2409
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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REGISTRATION NUMBER: 38,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/814,095
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                                                                                                                                    /evidence= EXPERIMENTAL
/gene= "ACHE"
                                                                                                                                                                                                                                                                           /evidence= EXPERIMENTAL
/gene= "ACHE"
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/gene= "ACHE"
/number= 2
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/gene= "ACHE"
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                                        experimental
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OTHER INFORMATION: /number= 5 FEATURE:
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION:
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LOCATION:
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LOCATION:
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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OTHER INFORMATION:
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                                  LOCATION: complement (31131..31284)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 11
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RMATION: /gene= "AR"
RMATION: /number= 2
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                                                                                                                                                                                                                                                                                              complement (31894..32080)
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                                                                                                                                                                                                                                                         8490 GGCTGGAGGGCAGTGGTGCGATCTCCGGCTCACTGCAACCTCTACCTCCTAGATTCAAGCA 8549
                                                                                                                                                                                                                                                                                                                                                                   1686 ttcgtaaacaattcactgcctgtttgtttgtttttttgagaaagtcttgctttgctctgttgc--- 1742
                                                                                                                                                                                                                                                                                                                                                                                                                             8370 CTTAAAAAGAAAAAAATAGATTTGGGGAAAAGTAGATCTTTATAGAGCCGAACACCTTTT 8429
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    8670 ACTCCTAACCTCAGGTGATCCACCCCACCTCGGCCTCTCAAAGTACTGGGATTACAGGCAT 8729
                              1923 actcctgacctcaagtgatctgcccaccttggcctcccaaagtgctgggattacagg--t 1980
                                                                                          8610 TAATTTTTTGTATTTTTAGTAGAGACAGGGTTTTGCCCATGTTGGCCAGGCTGGTCTTGA 8669
                                                                                                                                                                        1743 ggctggagtgcactggtgtgatgttggctcactgcaacctccacctcccaggctcaagtg 1802
                                                                                                                                                                                                                                                                                                                                            8430 TATTTATTTATTTATTTATTTATTTATTTTATTTTGAGACAGAGTCTCGCTGTGTTGCCCA 8489
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LOCATIÓN:
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
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LOCATION: complement (29664..29856)
OTHER INFORMATION: /gene= "ARS"
OTHER INFORMATION: /number= 16
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OTHER INFORMATION: /gene= "AR"
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 13
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Local Similarity 69.6%; Pred. No. 9e-67;
es 481; Conservative 0; Mismatches 177; Indels 33; Gaps
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
FILE REFERENCE: Davies Col
FILE REFERENCE: Davies Col
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Patent No. 6265211
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
                                                                            10151 GGGTTTTGCCATGTCGGCTAGGCTGGTCTTGAGCTCCTGGCTTCAAGTGATCCACCTGCC 10092
                                                                                                                                                                             10439 GTATGCCGAGACTGCGCCATTGCACTCCAGACTGGGCGACAGGGTGAGACTGTCTCAAAG 10380
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                                                                                                                                                                                                                                                                                  10270 CTGCAACCTCCACCTCCCAGGTTCAAGCAATTCTCATGTCTCAGCCTCCCAAGTAGCTGG 10211
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1951 ttggcctcccaaagtgctgggattacag--gtgagccacctcgcccagccagttcact 2006
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                                                                                                           1891 aagtttaatcatgtgggccaggctggttttgaactcctgacctcaagtgatctgcccacc 1950
                                                                                                                                                                                                              1834 gattacaggcgatttttttttacagttaatttttttttgttatttttcaggagagaca---a 1890
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Local Similarity 71.4%;
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1535 ccagctactcgggaggctgaggcaggagaatggcytgaacccgggaggcgaagcttgtag 1594
                                                                               1475 accccgtctctactaaaaatacaaaaaattagccgggcgtggtggcgggacgcctgtagtc 1534
                                                                                                                                                            1415 ggccgagatgggcttatcacgagatcaggagatcgagaccatcctagccaacatggggaa 1474
                                                                                                                                                                                                                                   1355 ttaaaatgccatttagggctgggcgcggtggctcacgcctgtaatcccagcactttggga 1414
                                                        3093 ACCCCGTCTCTACTAAAAATACAAAAATTAGCCGGGCGTAGTGGCGGGGGCGCCTGTAGTC 3152
                                                                                                                                                                                                                 2973 TAAAAAGTCTTTATAAGGCCGGGGCGCGCGCTGCCTCACGCCTGTAATCCCCAGCACTTTGGGA 3032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 415-576-0200
                                                                                                                                       3033 GGCCGAGGCGGCGGATCACGAGGTCAGGAGATCGAGACCATCCCGGCTAAAACGGTGAA 3092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                             Match 4.2%;
Local Similarity 90.6%;
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitts, Renee A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not relevant
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SYSTEM: PC-DOS/MS-DOS
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 Mismatches

                                                                                                                                                                                                                                                                                                             Score 270; DB 2;
Pred. No. 2.1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  017957-000100
                                                                                                                                                                                                                                                                                            30; Indels
                                                                                                                                                                                                                                                                                                                                  Length 246240;
                                                                                                                                                                                                                                                                                          0; Gaps
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US-08-724-394A-21; Sequence 21, Application US/08724394A
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                                                          В
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                                                                                                                                          Matches
                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 21:
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APPLICANT:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Megabase Transcript Map: No. 58'
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
                                                                                 1355 ttaaaatgccatttagggctgggcgggtggctcacgcctgtaatccccagcactttggga 1414
                 1415 ggccgagatgggcttatcacgagatcaggagatcgagaccatcctagccaacatggggaa 1474
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pa
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NAME: Fitts, Renee A.
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                                                          2973 TAAAAAGTCTTTATAAGGCCGGGCGCGCGCTGCCTCACGCCTGTAATCCCAGCACTTTGGGA 3032
                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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CLASSIFICATION: 536

TORNEY/AGENT THE US/08/724,394A
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                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1..246240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: not
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                       Match 4.2%;
Local Similarity 90.6%;
les 288; Conservative
                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "HLA-H.CONTIG"
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                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
DEDNESS: not relevant
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Wolff, Roger K.
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                                                                                                                                                                                                                                                                                                                                                             not relevant
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CDNA
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                                                                                                                                       0; Mismatches
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                                                                                                                                                           Score 270; DB 2; Length 246240; Pred. No. 2.1e-60;
                                                                                                                                          30; Indels 0; Gaps
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US-08-724-394A-22
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
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NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wollf, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 58'
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
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                                                                                FEATURE:
                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palanteners
        LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/01
FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
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                                                                                                                           TOPOLOGY:
                                                                                                                                          STRANDEDNESS:
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                                                          NAME/KEY: misc_feature
                                                                                                                                                                                   LENGTH:
                                                                                                                                                              nucleic acid
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                                                                                                                                                                                   246240 base pairs
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                                                                                                                      not relevant
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Best Local Similarity

4.2%; 90.6%;

Score 270; DB 2; Pred. No. 2.1e-60;

Length 246240;

Query Match

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US-08-694-915-5
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                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
         ANTI-SENSE:
                         MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adamou, Julie
APPLICANT: Kirkpatrick, Robert
APPLICANT: Rosenberg, Martin
TITLE OF INVENTION: HUMAN CARTI
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                                                                    TOPOLOGY:
                                                                                      STRANDEDNESS:
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COMPUTER: IBM CO
OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08629939; Patent No. 5645995; GENERAL INFORMATION:
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                                                                                                                    TELEFAX: (202) 293-7860 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kieback, TITLE OF INVENTION: TITLE OF INVENTION:
MOLECULE TYPE:
                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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                                    STRANDEDNESS:
                                                                                                                                                                                                                              REGISTRATION NUMBER: 30,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington,
                    TOPOLOGY:
                                                                TYPE:
                                                                             LENGTH:
                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                  (202) 293-7060
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US-08-759-873-5/c
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                                                                                                                           TELEPHONE: (202) 293-7060
TELEPHONE: (202) 293-7860
TELEPAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kieback, Dirk G.
TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED RISK
TITLE OF INVENTION: OF BREAST OR OVARIAN CANCER
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                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20037
COMPUTER READABLE FORM:
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HYPOTHETICAL:
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                                                 STRANDEDNESS:
                                                                           TYPE:
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                   NAME: KIT, Gordon REGISTRATION NUMBER: 30,764
                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 12-AP
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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                                  TOPOLOGY:
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                                                                                          CENGTH:
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                                                                                    320 base pairs
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; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 6
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APPLICANT: Hendrickson, Eric
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Patent No. 6171857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: B0877/7017/HK
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12354 GCTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTGAGCCGAGATCCCG 12295
                                                                                                                                                                                                                                                                                                                                                                                  12474 ATCACGAGGTCAGGAGATCGAGACCATCCCGGCTAAAACCGTGAAAACCTCGTCTCTACTA 12415
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                                  1550 gctgaggcaggagaatggcgtgaacccgggaggcgaagcttgtagtgagccgagatcgca 1609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1998-10-16
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-467-7176
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12234 AAA 12232
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                      1537 agctactcgggaggctgaggcaggagaatggcgtgaacccgggaggcgaagcttgtagtg 1596
                                                                                                      1477 cccgtctctactaaaaatacaaaaaattagccgggcgtggtggtggcggcctgtagtccc 1536
                                                                                                                                                                 8683 CCGAGGCGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACATGGTGAAAC 8742
                                                                                                                                                                                        1417 ccgagatgggcttatcacgagatcaggagatcgagaccatcctagccaacatggggaaac 1476
                                                                                                                                                                                                                                                     8623 AAGTAGACTTTCAGGGCCGGGCATGGTGGCTCACGCCTGTAATCCCCAGCACTTTGGGAGG 8682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/031,435
PRIOR DATE: 20-NOV-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Altier1, Dario C.
TITLE OF INVENTION: SURVIVIN, A PROTEIN THAT INHIBITS
TITLE OF INVENTION: CELLULAR APOPTOSIS, AND ITS MODULATION
NUMBER OF SEQUENCES: 35
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                                                                               8743 CCCGTCTTTACTAAAAATACAAAAAATTAGCTGGGCGTGGTGGCGGCGCCTGTAGTCCC 8802
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 20-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin p-''
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                       Match 4.1%;
Local Similarity 90.4%;
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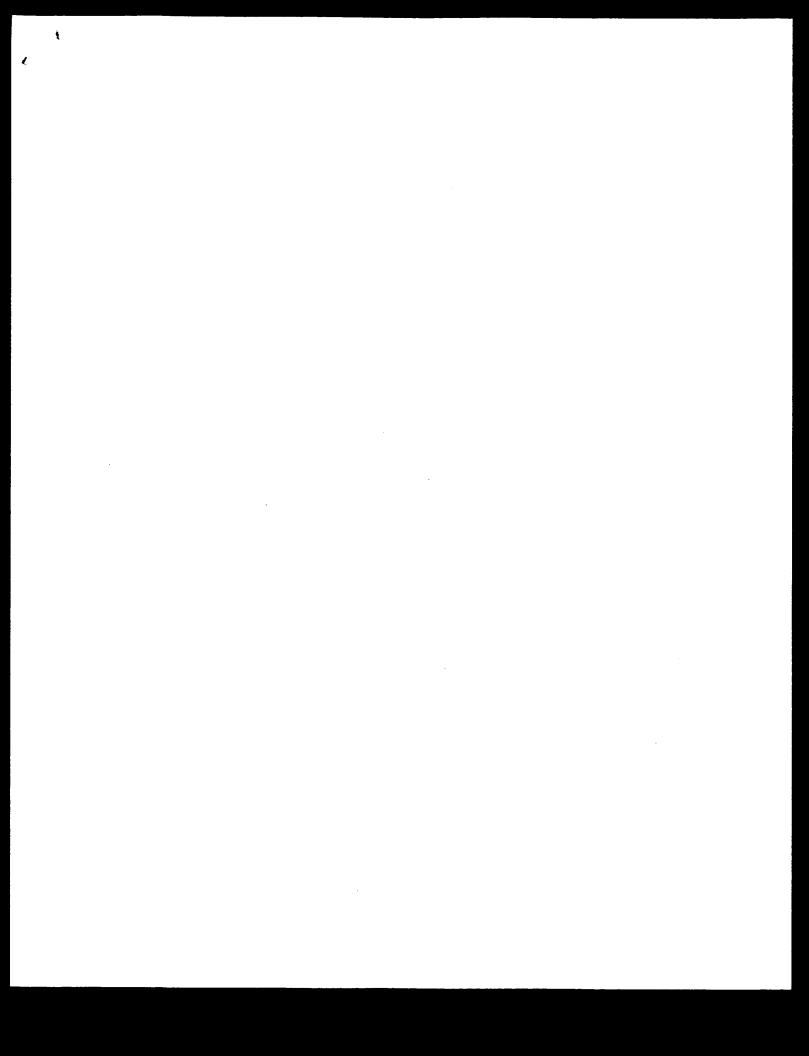
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SEQ ID NO 10
LENGTH: 14796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTISENSE MODULATION FILE REFERENCE: RTS-0053 CURRENT APPLICATION NUMBER: US/09/630,706 CURRENT FILING DATE: 2000-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: C. Frank Bennett
APPLICANT: Lex M. Cowsert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: NAME/KEY: CDS
NAME/KEY: (5158)...(5275)
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LOCATION: (31
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LOCATION: (11)
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                                                                        8863 agecgagategegecaetgeaeteeageetgggegaeagagegagaeteegteteaaaaa 8922
                                                                                                                                                                                                                                8683 ccgaggcgggtggatcacgaggtcaggagatcgagaccatcctggctaacatggtgaaac 8742
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                                                                                                                                                   8803 agctactcgggaggctgaggcaggagaatggcgtgaacctgggaggtggagcttgctgtg 8862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 263; DB 4; Length 14796; 90.4%; Pred. No. 2.3e-59; rative 0; Mismatches 30; Indels 0;
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Maximum DB seq length: 2000000000
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Perfect score:
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  November 29, 2001, 05:49:45; Search time 6128.19 Seconds (without alignments) 11373.198 Million cell updates/sec
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6486
1 tcctcctcctcccccctc.....ggtccattcagcagcaggac 6486
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

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348.2	371.8	373.4	379.8	403.4	427.4	451.8	456	473.6	476.4	606.6	664.4	Score
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457	525	376	398	407	468	456	481	508	495	657	674	Match Length DB
13	10	10	10	10	13	10	13	10	10	10	10	!
AQ518451	AI250843	AI832007	AW292092	AI224367	B47140	AI379831	AQ391334	AA825207	AW575965	AW370369	AW978572	ID
AQ518451 HS_5101_A	AI250843 qx10a04.x	AI832007 wj99a02.x	AW292092 UI-H-BI2-	AI224367 qx05f07.x	B47140 HS-1068-B1-	AI379831 te29a09.x	AQ391334 CITBI-E1-	AA825207 oc66e07.s		AW370369 RC1-BT025	AW978572 EST390681	Description

AI431303 ar55a07.x	AI431303	10	423	4.1	9	45	G
PCI11	B48415	13	587	4.1	266.6	44	C
AV728425 AV728425	AV728425	10	693		₫.	43	
CITBI-E1	AQ395455	13	612		267	42	C
AQ528700 RPCI-11-3	AQ528700	13	551	4.1	267	41	
x172f11.	AW193265	10	368		267	40	C
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AV760777	AV760777	10	621		9	ω ω	
IT-HSP-21	в89781	13	444		3	32	
qt68h12	AI281881	10	405		33	31	a
CIT-F	AQ044082	13	394		3	30	
HS_5	AQ749821	13	766		5	29	
CIT-F	AQ002001	13	514		9	28	
RPCI1	AQ343449	13	664		270	27	
RPCI-	AQ483367	13	540		٠,	26	C
B16472 342F6.TPB C	B16472	13	630	4.2	270.2	25	C
qu23h	AI284640	10	337			24	
60231	BG249643	11	822		71	23	
CIT-F	AQ111077	13	675	٠	272.2	22	
RPCII	AQ380625	13	640		72	21	
DKFZ	AL046409	10	517		73	20	C
HS_22	AQ129641	13		•	8	19	a
260L1	AQ839854	<u>1</u> 3	14771		84	18	a
CIT-F	AQ019249	13	515		9	17	
qx04c	AI250350	10	300	•	298	16	C
ti41c	AI434322	10	315		304	15	C
00666	AA825205	10	338	4.7	306.8	14	O
wq64∈	AW003249	10	328		97	13	a

ALIGNMENTS

BASE COUNT ORIGIN	Tee Fai	TITLE Ass met JOURNAL Unj COMMENT COI	EUH MAN REFERENCE 1 AUTHORS Hee , I.	RESULT 1 AW978572/c LOCUS DEFINITION EST3: ACCESSION AW97! VERSION AW97! VERSION EST. SOURCE bundat ORGANISM Homo
/db_xref="taon:9606" /db_xref="taon:9606" /clone_lib="MAGE resequences, MAGP" /note="Vector: pBluescriptSKm" 185 a 178 c 191 g 120 t	Tel: 301 838 3528 Fax: 301 838 0208 Fax: 301 838 0208 Plate: 394 Plate: Forward. Location/Qualifiers 1. 674	Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) Contact: John Quackenbush The Institute for Genomic Research	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 674) Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt (J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and (Dhackenbush, J.	8572 674 bp mRNA 90681 MAGE resequences, M 8572 8572.1 GI:8169840

Matches 668; Conservative

Local Similarity

Query Match

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6197 ctgcacagtggggagcatggagggatgggttttggcctgtgcttctgcttattcagtcctt 6256
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            Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                 HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eufeleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                         AW370369 657 bp mrNA EST 04-FEB-2000 RC1-BT0255-181099-012-f04 BT0255 Homo sapiens cDNA, mRNA sequence.
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6289 tgacctcacagtactggttaattaaactttattgctc 6325
                                                                  6229 ggcctgtgcttctgcttattcagtccttcagctcacggaagggatgctagtccgtgaagg 6288
                                                                                                                                                        5989 coagccaggcctccagcacccccagtgcagctcgtgattggaaactcaccatcggcaggc 6048
                                                                                                                                                                                                                                                                                                                                          6049 agtggttcggttttaagaggatggcattagagggagcccagtctggatgtggacttgggatgc 6108
                                         117 GGCCTGTGCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGATGCTAGTCCGTGAAGT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5809 tcccactcaggtctgtacttagggcagctggcctggatgggcttcactggggccctgtct 5868
                                                                                                                                  177 ATGTACACCAGAGCCTCAGTGAGCCCATCTGCACAGTGGGGGAGCATGGAGGGATGGGTTT 118
                                                                                                                                                                                                                        297 AGTGGTTCGGTTTAAGAGATGGCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 GCAGTAGGGCCCCTGCACACTCAGTTTCTCTCGTTTTTCCTTAGTTATCAGTCCTGTCCTG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCATGCTGATCTTCTAGATGCCACTCCCAAATCCCCTTCATACCCACCAGGATGTGTGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcatgctgatcttctagatgccactcccaaatccccttcatacccaccaggatgtgtgc 5988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCCCACTCAGGTCTGTACTTAGGGCAGCTGGCCTGGATGGGCTTCACTGGGGCCCTGTCT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC1&t2=RC1-BT0255-181099-012-f04&t3=1999-10-18&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="organ: breast; vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.716 Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="BT0255"
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SOURCE ORGANISM

Homo sapiens

KEYWORDS VERSION DEFINITION

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AW370369.1 GI:6875023

ACCESSION

AW370369/c

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14 TTATTGCTCCCTGT 1

6317 ttattgctcactgt 6330

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REFERENCE

(bases 1 to 657)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
6034 tcaccatcggcaggcagtggttcggtttaagaggtggcattagagggggcccagtctgga 6093
                                                                                                                                                                                                                                                                           5974
                                                                                                                                                                                                           5914 ttctcctctgtgcccctcatgctgatcttctagatgccactcccaaatccccttcatacc 5973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                         435
                                                                                                                                                                                                                                                       57 GACCTCACAGTACCTGGTTAATTAAACTTTATTGCTC 21
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                           caccaggatgtgtgcccagccaggcctccagcacccccagtgcagctcgtgattggaaac 6033
                                                                                                                                                                CACCAGGATGTGTGCCCAGCCAGGCCTCCAGCACCCCCAGTGCAGCTCGTGATTGGAAAAC 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortim/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UI-HF-BL0-acn-h-03-0-UI.s1 NIH_MGC_37 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
131 c 129 g 109 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (LTI)"
/note="Vector: pT713-Pc; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT713-Pc; Site_1: Not1; Site_2: Eco RI;
/note-"Vector from size fractionated cytoplasmic mRNA
(1.5-2.5kb). Directionally cloned. Cells provided by Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3059932"
/clone_lib="NIH_MGC_37"
/tissue_type="lymph"
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99.4%;
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_line="MGC85"
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Pred. No. 3.8e-48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6094 tgtggacttggatgccctgtgggtatcagttctgctgacactttggcccgaaatagatcc 6153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 449.
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AA825207
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Insert Length: 1099 Std Error: 0.00
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DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Warti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
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     125 a
                                                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo."
1 129 c 132 g 122 t
                                                       (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="IMAGE:1354692"
                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="germinal center B cell"
/lab_host="DH10B"
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                                                                                                                                Double-stranded cDNA was ligated to Eco RI adaptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328 TCACCATCGGCAGGGAGTGGTTCGGTTTAAGAGATGCCATTACAGGGAGCCCAGTCTGGA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448 TTCTTCTCTGTGCCCCTCATGCTGATCTTCTAGATGCCACTCCCAAATCCCCTTCATACC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 TGGAGGGATGGGTTTGGCCTGTGCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGAT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 AGTGCTGAGCAATGTACACCGGAGCCTCAGTGAGCCCATCTGCACAGTGGGGGAGCA 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITBI-E1-2554019.TR CITBI-E1 Homo sapiens genomic clone 2554019,
                                                                                                                                                                                                                               Seq primer: M13 Reverse Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA sequence.
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                                                                                                                                                                                                                                                                                                                                               end search page:
                                                                                                                                                                                                                                                                                                                                                                                        Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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301 838 0208
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BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                              hbe@tigr.org
                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                      Location/Qualifiers
/clone_lib="CITBI-E1"
                                         /clone="2554019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Dr., Rockville, MD 20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGAATACTCAGCTTTAACCCAAGGTGTTGACAGGTTGGAAACAGTGGCTAAATTTGGGGA 122
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                                                                                                                                                                                              Insert Length: 746 Std Erro
Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI379831
                                                                                                                                                     High quality sequence stop: 455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI379831.1 GI:4189684
                                                                                                                                                                                                                                                                         IMAGE Consortium (info@image.llnl.gov) for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 456)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Cell_type="sperm"
/Cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_1: Ec
    /db_xref="taxon:9606"
                                     /organism="Homo sapiens"
                                                                                                           location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%;
98.7%;
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 Mismatches

                                                                                                                                                                                                                                   Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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B47140/c
                                                                                                                        REFERENCE
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                                                                                                                                                                                                                                                            KEYWORDS
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                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 453; Conservative
                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6239 tctgcttattcagtccttcagctcacggaagggatgctagtccgtgaaggtgacctcaca 6298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6299 gtactggttaattaaactttattgctcactgtcca 6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6059 tttaagagatggcattagagggagcccagtctggatgtggacttggatgccctgtgggta 6118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 GAGCCTCAGTGAGCCCATCTGCACAGTGGGGAGCATGGAGGGATGGGTTTGGCCTGTGCT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 TTTAAGAGATGGCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 GTACTGGTTAATTAAACTTTATTGCTCACTGTCAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gagcctcagtgagcccatctgcacagtggggagcatggagggatgggtttggcctgtgct 6238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGATGCTAGTCCGTGAAGGTGACCTCACA 37
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 468)

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                      B47140 468 bp DNA GSS 21-OCT-1997
HS-1068-B1-B10-MR.abi CIT Human Genomic Sperm Library C Homo
saptens genomic clone Plate=CT 278 Col-19 Row-D, DNA sequence.
                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                        B47140.1 GI:2551974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE: 2087320"
/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 451.8; DB 10; Length 456; Pred. No. 3.4e-45;
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                                                            KEYWORDS
                                                                                  VERSION
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                          ORGANISM
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                                                                                                                                                                                                                                                                                  1560 gagaatggcgtgaacccgg-gaggcgaagcttg 1591
                                                                                                                                                                                                                                                                                                                                                                                                                                        1440 caggagatcgagaccatcctagccaacatggggaaaccccgtctctactaaaaatacaaa 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1380 cggtggctcacgcctgtaatcccagcactttgggaggccgagatgggcttatcacgagat 1439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1200 atcacttcaagctctgctttttgggaactttgtggaattttctttttttccccaaatatttt 1259
                                                                                                                                                                                                                                                                                                                                                                1500 aaattagccgggcgtggtggcggacgcctgtagtcccagctactcgggaggctgaggcag 1559
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                                                                                                                                                                                                                                                                                                                                          109 AAATTAGCCGGGCGTGGTGGCGGACGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAG 50
                                                                                                                                                                                                                                                                                                                                                                                                                         169 CAGGAGATCGAGACCATCCTAGCCAACATGGGGAAACCCCGTCTCTACTAAAAATACAAA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 CGGTGG-TCACGCCTGTAATCCCCAGCACTTTGGGAGGCCGAGATGGGCCTTATCACGAGAT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                288 CCTTAGTGTAATGTGGTAAAAGCATATCCGGATATTTAAAATGCCATTTAGGGCTGGGCG 229
                                                                                                                                                                                                                                                                49 GAGAATGGCGTGAACCCGGCGAGGCGAAGCTTG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
                 Homo sapiens
                                                               EST
                                                                                                                                      qx05f07.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2000485 3',
                                                                                                                                                              AI224367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Tagged Connector
Plate: CT 278 row: D cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: (206) 616-8744
Fax: (206) 685-7301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tagged Connectors
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                AI224367.1 GI:3807080
                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: kzackron@u.washington.edu
                                           nman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="CIT Human Genomic Sperm Library C"/sex="M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="Plate=CT 278 Col=19 Row=D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%;
99.3%;
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Pred. No. 2.8e-42;
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                                                                                                                                                                 mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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DEFINITION
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                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 404; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6169 atgtacaccggagcctcagtgagcccatctgcacagtggggagcatggagggatgggttt 6228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5989 ccagccaggcctccagcacccccagtgcagctcgtgattggaaactcaccatcggcaggc 6048
                                                                                                                                                                                                                                                                                                    6289 tgacctcacagtactggttaattaaactttattgctcactgtcca 6333
                                                                                                                                                                                                                                                                                                                                                                                                        6229 ggcctgtgcttctgcttattcagtccttcagctcacggaagggatgctagtccgtgaagg 6288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6049 agtggttcggtttaagagatggcattagagggagcccagtctggatgtggacttggatgc 6108
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                                                                                                                                                                                                                                                                                                                                                                     107 GGCCTGTGCTTCTGCTTATTCAGTCCTTCAGCTCACGGAAGGGATGCTAGTCCGTGAAGG 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          407 CTCATGCTGATCTTCTAGATGCCACTCCCAAATCCCCTTCATACCCACCAGGATGTGTGC 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 CCAGCCAGGCCTCCAGCACCCCCAGTGCAGCTCGTGATTGGAAACTCACCATCGGCAGGC 288
                                                                                                                                                                                                                                                                                 47 TGACCTCACAGTACTGGTTAATTAAACTTTATTGCTCACTGTCAA 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGTACACCGGAGCCTCAGTGAGCCCATCTGCACAGTGGGGAGCATGGAGGGATGGGTTT 108
                                                                                                                           UI-H-BI2-agx-a-12-0-UI.sl NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2725559 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 407)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                       Homo sapiens
                                                                                     AW292092.1 GI:6698728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
                                         numan
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Similarity 99.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"

a 109 c 107 g 91 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE: 2000485"
/clone_lib="NCI_CGAP_Lym12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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                                                                                                                                                                       398 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 403.4; DB 10;
Pred. No. 2.2e-39;
                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                         16-JAN-2000
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                                                                                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                     BASE COUNT
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                                                                                                        Matches 381;
                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                          source
                       The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLYA=Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
                                                                                                        Conservative
                                                                                                                                                                                                                                     92 a
                                                                                                                                                                                                                                                                                                                                                                                               TAG_LIB=NCI_CGAP_Lu5
TAG_TISSUE=lung
TAG_SEQ=CAAC"
                                                                                                                                                                                                                                                                                                                    Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Sub4"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2725559"
                                                                                                                                                                                                                                                                                                                                                                ) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                        5.9%;
                                                                                                                                                                                                                                     104 c
                                                                                                        0;
                                                                                        Score 379.8; DB 10; Long
Pred. No. 1.5e-36;
Pred. No. 1.5e-36; Indels
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KEYWORDS
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                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
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                         Best Local Similarity
                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6131 acactttggcccgaaatagatccagtgctgagcaagcaatgtacaccggagcctcagtga 6190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6311 taaactttattgctcactgtcca 6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6251 gtccttcagctcacggaagggatgctagtccgtgaaggtgacctcacagtactggttaat 6310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6071 cattagagggagcccagtctggatgtggacttggatgccctgtgggtatcagttctgctg 6130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GCCCATCTGCACAGTGGGAGCATGGAGGGATGGGTTTGGCCTGTGCTTCTGCTTATTCA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38 TAAACTTTATTGCTCACTGTCAA 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATTACAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCTG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI832007 376 bp mRNA EST 41-DEC-1995 wj99a02.xl NCI_CGAP_Lym12 Homo sapiens cDNA clone INAGE:2410922 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11547-015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 375.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
       Conservative
                                                                                                                                            /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
a 105 c 97 g 82 t
                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE: 2410922"
/clone_lib="NCI_CGAP_Lym12"
                                                                                                                                                                                                                                                                                                              /tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                            5.8%;
99.7%;
  0; Mismatches
                         Score 373.4; DB 10; Length 376; Pred. No. 8.9e-36;
     0;
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AI250843/c
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                                                                                                                                            BASE COUNT
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                         Query Match 5.7%;
Best Local Similarity 99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
Matches 373; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6317 ttattgctcactgtc 6331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6197 ctgcacagtggggagcatggagggatgggtttgggcctgtgcttctgcttattcagtcctt 6256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6137 tggcccgaaatagatccagtgctgagcaagcaatgtacaccggagcctcagtgagcccat 6196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6077 agggagcccagtctggatgtggacttggatgccctgtgggtatcagttctgctgacactt 6136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6017 agctcgtgattggaaactcaccatcggcaggcagtggttcggtttaagagattggcattag 6076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 CTGCACAGTGGGGAGCATGGAGGGATGGGTTTGGCCTGTGCTTCTGCTTATTCAGTCCTT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196 TGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCAT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 AGCTCGTGATTGGAAACTCACCATCGGCAGGCAGTGGTTCGGTTTAAGAGATGGCATTAG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 AGGGAGCCCAGTCTGGATGTGGACTTTGGATGCCCTGTGGGTATCAGTTCTGCTGACACTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TTATTGCTCACTGTC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 336
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
unknown library type
Insert Length: 1149 Std Er
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 525)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Index
                                                                                                                                                                 /note-"Organ: lymph node; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015"
                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="ImAGE:200910"
/clone=lib="NCI_CGAP_Lym12"
/clone_lib="NCI_CGAP_Lym12"
/tisue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                  /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ518451 457 bp DNA GSS 05-MAY-1999 HS_5101_A2_E10_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=677 Col=20 Row=I, DNA sequence.
                                                                                                                                                                                                                                                                                                                  Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pleter de Jong
library availability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                       High quality sequence stop: 457
                                                                                                                                                                                                                                                                       http://www.htsc.washington.edu
Plate: 677 row: I column: 20
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Lodger, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Lodger, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Lodger, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                          Seq primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High Throughput Sequencing Center University of Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (206) 616-3887
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                            /clone_lib="RPCI-11 Human Male BAC Library"
                                                      /db_xref="taxon:9606"
/clone="Plate=677 Col=20 Row=I"
                                                                                                            /organism="Homo sapiens"
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Insert Length: 384 Std Erro
Seg primer: -40UP from Gibco.
                                                                    DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                    cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                          Emmert-Buck, M.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6190 agcccatctgcacagtgggggagcatggagggatgggttttggcctgtgcttctgcttattc 6249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6070 gcattagagggagcccagtctggatgtggacttggatgccctgtgggtatcagttctgct 6129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 AGCCCATCTGCACAGTGGGAGCATGGAGGGATGGGTTTGGCCTGCTTCTGCTTATTC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          268 GCATTAGAGGGAGCCCAGTCTGGATGTGGACTTGGATGCCCTGTGGGTATCAGTTCTGCT 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320; Conservative
                                     Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman,
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oc66e05.sl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1354688 3',
                             Bonaldo, Ph.D.
                                                                                                                                                                                                           National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA825205
cDNA Library Arrayed by: Greg Lennon, Ph.D.
                                                                                                                                                                                                                                                                           (bases 1 to 338)
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                                                                                                                                                                                                     Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. " a 95 c 73 g 76 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: p1713D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE: 2476070"
/clone_lib="NCI_CGAP_GC6"
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/db_xref="taxon:9606"
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DEFINITION
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                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.7%; Score 306.8; DB 1
Best Local Similarity 99.4%; Pred. No. 8.5e-28;
Matches 308; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                   6324 tcactgtcca 6333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6204 gtggggagcatggagggatgggtttggcctgtgcttctggcttattcagtccttcagctca 6263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6144 aaatagatccagtgctgagcaagcaatgtacaccggagcctcagtgagcccatctgcaca 6203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6024 gattggaaactcaccatcggcaggcagtggttcggtttaagagatggcattagagggagc 6083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 AAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCATCTGCACA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     338 GATTGGAAACTCACCATCGGCAGGCAGTGGTTCGGTTTAAGAGATGGCATTACAGGGAGC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 GTGGGGAGCATGGAGGGATGGGTTTGGCCTGCTTCTGCTTATTCAGTCCTTCAGCTCA 99
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                                                                                                                                                                                                                                                                                                                                                        38 TCACTGTCAA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                         ti41d01.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2133025 3',
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         mRNA sequence.
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                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 135.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             j. Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Nu
and Eco RI sites of the modified p7773 vector. Library
went through one round of normalization, and was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand of was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
/note="Variation"
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/db_xref="taxon:9606"
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search completed: November 29, 2001, 05:50:11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                          6136 ttggcccgaaatagatccagtgctgagcaagcaatgtacaccggagcctcagtgagccca 6195
                                                                                                                       6316 tttattgctcactgtc 6331
                                                                                                                                                                                                                                                                                                                                 196 TTGGCCCGAAATAGATCCAGTGCTGAGCAAGCAATGTACACCGGAGCCTCAGTGAGCCCA 137
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                                                                                                 TTTATTGCTCACTGTC 1
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Life Technologies catalog #: 11547-015

LNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: WCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1751 Std Error: 0.00

Seq primer: 40UP from Gibbo

Seq primer: 40UP from Gibbo
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.25 kb. Life Technologies catalog #: 11547-015" 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="lymphoma, follicular mixed small and large
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/clone_lib="NCI_CGAP_Lym12"
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